COVID-3D

Browse   User variants   Help   Tutorials   Code   Contact   Acknowledgements

Surface glycoprotein (Spike) (Uniprot: P0DTC2 - GenBank: QHD43416)
Related resources

MTR: **0.85 (Intolerant)** / RVIS: **-0.14 (Intolerant)**

3D Structure

Structure ⓘ

[Closed   ▾]

Pockets ⓘ

Background ⓘ   Representation   Color Scheme ⓘ   #1 - Volume
[White   ▾]   [Cartoon   ▾]   [Secondary Structure▾]   62395.395 Å³   EasyVS

☐ Pocket ⓘ   ☐ Surface ⓘ   Fragment Hotspots ⓘ:   ☐ Acceptor
                                                 ☐ Donor   ☐ Apolar
☐ COVID-19 Variants ⓘ
☐ Variant Frequency ⓘ
☐ Evolutionary Coupling ⓘ

☐ Mutations from SARS ⓘ
☐ Mutations from Bat RaTG13 ⓘ

Opacity: 0.6

COVID-3D

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Related resources

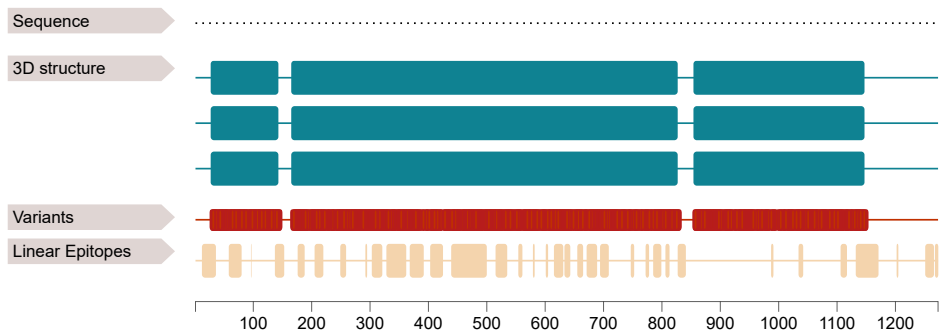| C | SPIN | 📷 | ⛶ | ❓ HELP |

Sequence

❓ HELP

Position : 0   **Zoom :** x 1

Sequence

3D structure

Variants

Linear Epitopes

| 100   200   300   400   500   600   700   800   900   1000   1100   1200 |

Mutational Tolerance (Missense Tolerance Ratio)

COVID-3D

Horizontal lines show gene-specific MTR percentiles 5th, 25th, 50th, and neutrality (MTR = 1.0)
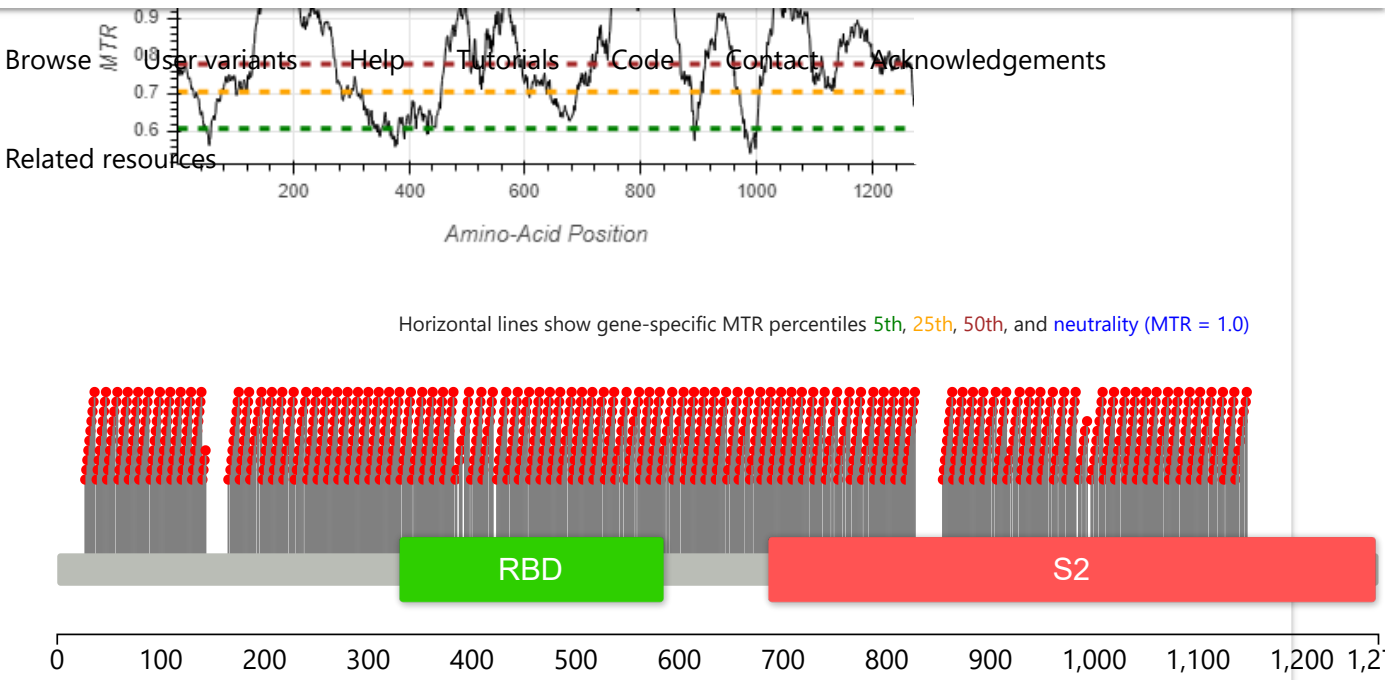
Mutations   ANALYSIS [↗]   SATURATION MUTAGENESIS [↗]

ⓘ

- ☐ Residue Properties
- ☐ Stability/Affinity Scores
- ☐ PSSM Scores
- ☐ AAindex
- ☐ Clade Frequency
- ☐ Contacts

SARS-CoV2 Circulating Variants

Show [10 ▾] entries

Search:

Position ↑↓	AA from ↑↓	AA to ↑↓	Chain ↑↓	Frequency (%) ↑↓	Depth (Å) ↑↓	Details	) ↑↓	Psi (°) ↑↓	RSA (
27	A	S	A	0.07	1.94	[↗]		161.2	0.69
27	A	V	A	0.04	1.94	[↗]		161.2	0.69
27	A	S	B	0.07	1.95	[↗]		160.9	0.7

↑↓ ↑↓ ↑↓ ↑↓ ↑↓ ↑↓ ↑↓ ↑↓ ↑↓

COVID-3D

Position	AA from	AA to	Chain	Frequency (%)	Depth	Details		Psi (°)	RSA
27	A	V	C	0.04	1.97			160.1	0.7
27	A	E	A	< 0.01	1.94	🔗		161.2	0.69
27	A	E	B	< 0.01	1.95	🔗		160.9	0.7
27	A	E	C	< 0.01	1.97	🔗	---	160.1	0.7
27	A	K	A	< 0.01	1.94		360	161.2	0.69

PREVIOUS   1   2   3   4   5   …   870   NEXT

Mutations from SARS ⓘ

Show [10 ˅] entries

Search:

Position ↑↓	AA from ↑↓	AA to ↑↓	Chain ↑↓	Frequency (%) ↑↓	Depth (Å)	Details ↑↓	↑↓	Psi (°) ↑↓	RSA
127	V	A	A	< 0.01	2.69	🔗		132.5	0.2
127	V	A	B	< 0.01	2.67	🔗		131.4	0.2
127	V	A	C	< 0.01	2.7	🔗		131.3	0.2
194	F	L	A	< 0.01	4.22	🔗		124.4	0.01
194	F	L	B	< 0.01	4.22	🔗		124.2	0.01
194	F	L	C	< 0.01	4.23	🔗		124.2	0.01
618	T	A	A	< 0.01	1.85	🔗		-41.9	0.63
618	T	A	B	< 0.01	1.9	🔗		-35	0.52
618	T	A	C	< 0.01	1.91	🔗		-33.6	0.52
687	V	I	A	< 0.01	1.93	🔗	-85.2	96.6	0.89

Showing 1 to 10 of 15 entries

PREVIOUS   1   2   NEXT

Mutations from Bat RaTG13 ⓘ

Show [10 ˅] entries

Search:

COVID-3D

Browse | Position | User variants | Help | Tutorials | Frequency (%) | Code | Contact Depth (Å) | Acknowledgements | PSIC | RSA

Related resources

Position	aa	aa	Code	Frequency (%)	Depth (Å)			PSIC	RSA
32	F	S	A	< 0.01	3.07	⬈		-110.4	0.18
32	F	S	B	< 0.01	3.07	⬈		-110.5	0.17
32	F	S	C	< 0.01	3.07	⬈		-110.6	0.17
50	S	L	A	0.01	1.79	⬈		135.2	0.37
50	S	L	B	0.01	1.79	⬈		135.2	0.36
50	S	L	C	0.01	1.79	⬈		135.1	0.35
76	T	I	A	0.06	1.88	⬈		152.1	0.42
76	T	I	B	0.06	2.2	⬈		136.7	0.51
76	T	I	C	0.06	1.92	⬈	)	6.3	0.63
218	Q	P	A	< 0.01	1.79	⬈	-69.8	142.2	0.71

Showing 1 to 10 of 48 entries

PREVIOUS   1   2   3   4   5   NEXT

Normal Mode Analysis

Porcupine Plots ⓘ
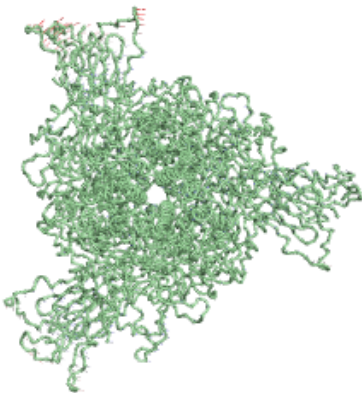
COVID-3D
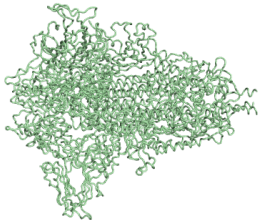
Browse   User variants   Help   Tutorials   Code   Contact   Acknowledgements
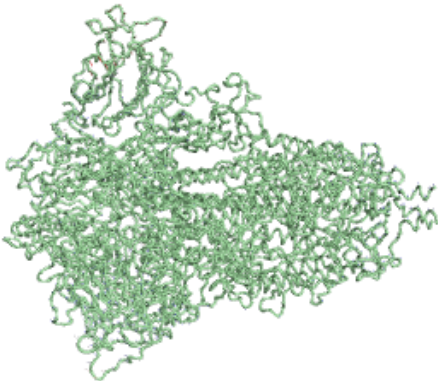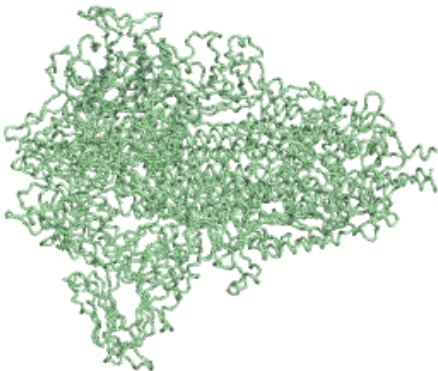
Related resources

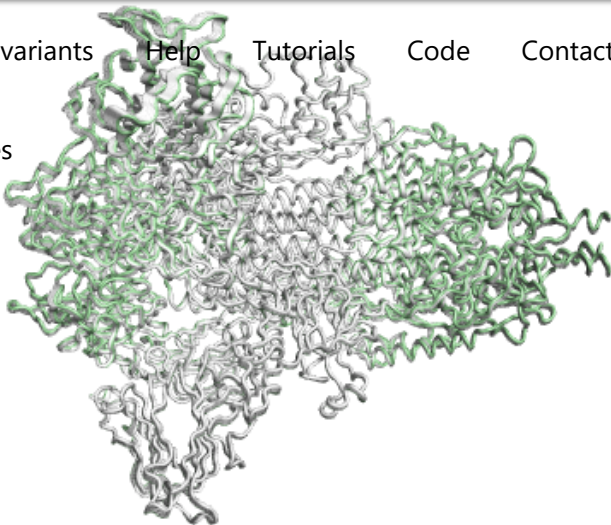## Modes Visualisation ⓘ

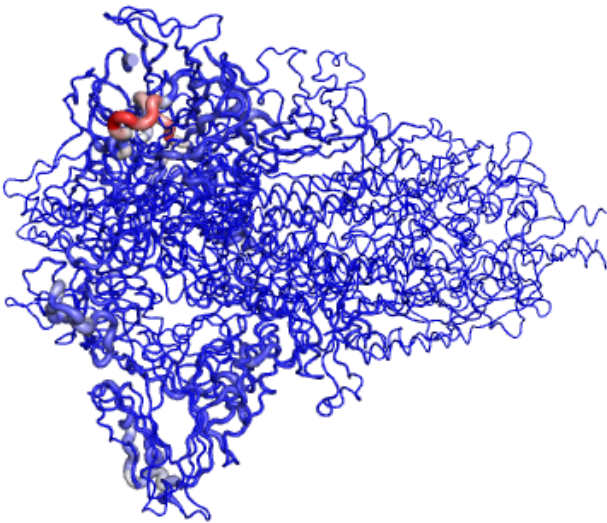# COVID-3D

Browse   User variants   Help   Tutorials   Code   Contact   Acknowledgements
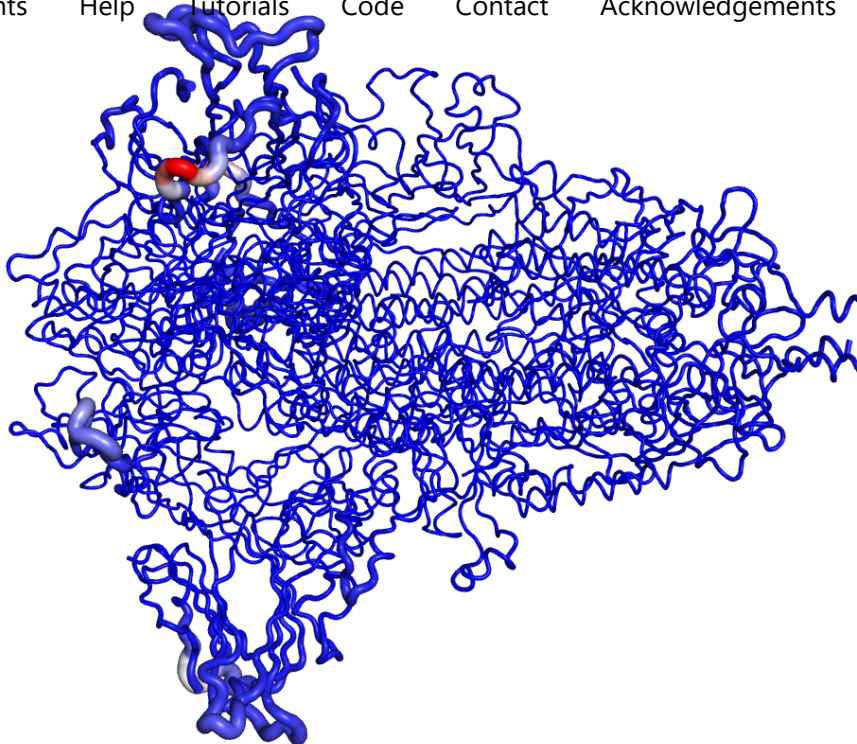
Related resources

Deformation Energy ⓘ

Atomic Fluctuation ⓘ

COVID-3D

Molecular Dynamics

COVID-3D - Surface glycoprotein (Spike) …

COVID-3D

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        User variants   Tutorials

Related resources

Biosig Lab

Structure

Our group is interested in developing and experimentally validating
Sequence
novel computational methods to exploit this data, enhancing the
impact of large scale sequencing, structural genomics, and functional
Mutations
genomics on biology and medicine.

NMA

MD

Downloads